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Terms	Documents
HSP70 same arthritis	10

Database:

US Patents Full-Text Database
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Search:

L14

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<u>Set Name</u> side by side	<u>Query</u>	<u>Hit Count</u>	<u>Set Name</u> result set
<i>DB=USPT,PGPB,DWPI; THES=ASSIGNEE; PLUR=YES; OP=OR</i>			
<u>L14</u>	HSP70 same arthritis	10	<u>L14</u>
<u>L13</u>	HSP?? same arthritis	59	<u>L13</u>
<u>L12</u>	HSP?? and arthritis	350	<u>L12</u>
<u>L11</u>	L9 and (HSP70 same arthritis)	4	<u>L11</u>
<u>L10</u>	L9 and (HSP same arthritis)	1	<u>L10</u>
<u>L9</u>	L8 and @RLAD<19981008	73	<u>L9</u>
<u>L8</u>	HSP70 and arthritis	174	<u>L8</u>
<u>L7</u>	burmester-gerd-r.in.	2	<u>L7</u>
<u>L6</u>	L1 and arthritis	125	<u>L6</u>
<u>L5</u>	wehlan-helmut.in.	0	<u>L5</u>
<u>L4</u>	anti-Bip-antibodies	0	<u>L4</u>
<u>L3</u>	L1 same arthritis	1	<u>L3</u>
<u>L2</u>	L1 sme arthritis	45648	<u>L2</u>
<u>L1</u>	Bip or GRP78	1692	<u>L1</u>

END OF SEARCH HISTORY



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GeneCard for gene HSPA5
GC09M119111

Approved [UCL/HGNC/HUGO Human Gene Nomenclature database](#) symbol
HSPA5 (heat shock 70kDa protein 5 (glucose-regulated protein, 78kDa))

**Aliases and Additional
Descriptions**
(According to [GDB](#), [HUGO](#),
and/or [SWISS-PROT](#))

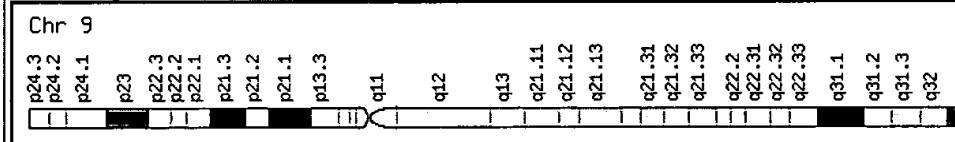
- BiP
- **GRP78**
- heat shock 70kD protein 5 (glucose-regulated protein, 78kD)
- heat shock 70kDa protein 5 (glucose-regulated protein, 78kDa)
- 78 kDa glucose-regulated protein precursor (GRP 78) (Immunoglobulin hea

Chromosomal Location
(According to [UDB/GeneLoc](#)
and/or [HUGO](#), and/or
[LocusLink](#),
Genomic Views According to
[UCSC](#) and [Ensembl](#))

Chromosome: 9 [UDB/GeneLoc gene densities](#)

LocusLink cytogenetic band: 9q33-q34.1 [Ensembl cytogenetic band: 9q33.3](#)

Gene in genomic location: bands according to Ensembl, locations according to UI



Unified DataBase (GeneLoc) location for GC09M119111: (about GC identifiers)

Start: 119,111,854 bp from *pter*

End: 119,118,331 bp from *pter*

Size: 6,477 bases

Orientation: minus strand

Unified DataBase (version 2.5) coordinate (from *pter*): [143.335 mega bases](#)

Genomic View:
[UCSC Golden Path](#)

Proteins
(According to [SWISS-PROT](#)
and/or [MIPS](#))

GR78 HUMAN

Size: 654 amino acids; 72333 Da

Function: PROBABLY PLAYS A ROLE IN FACILITATING THE ASSEMBLY OF

Subcellular location: Endoplasmic reticulum lumen.

Similarity: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.

MIPS Pedant Viewer: [72428](#)

REFSEQ proteins: [NP_005338.1](#)

**Protein
Domains/Families/Ontologies**
(According to [InterPro](#), [GO](#),
and/or [BLOCKS](#))

InterPro Domains and Families:

[IPR001023; Hsp70](#)

[IPR000886; ER target](#)

[Graphical View of Domain Structure for SP Entry P11021](#)

Gene Ontology (GO) terms (tree view):

[GO:0005524](#)

GO:0008077

GO:0005788

Blocks protein family: [IPB001023](#) Heat shock protein hsp70REFSEQ mRNAs: [NM_005347.2](#)

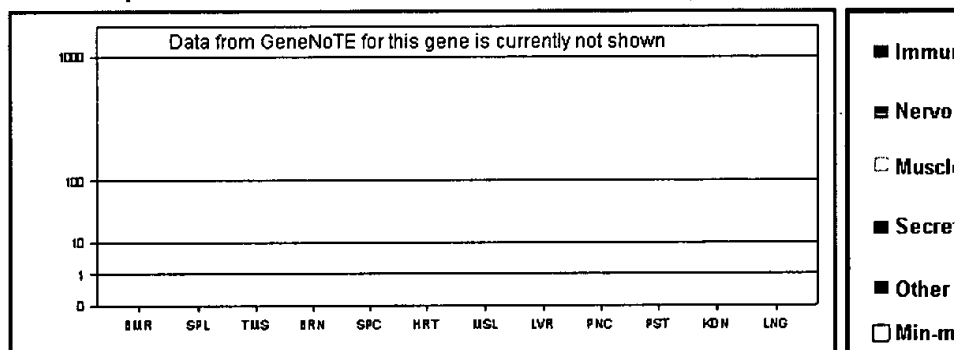
Additional Gene/cDNA sequence:

[AF216292](#) [AF216292.1](#) [AJ271729](#) [AJ271729.1](#) [BC020235](#) [BC020235.1](#) [M19X87949.1](#)MIPS assembly: [H56456S1](#)

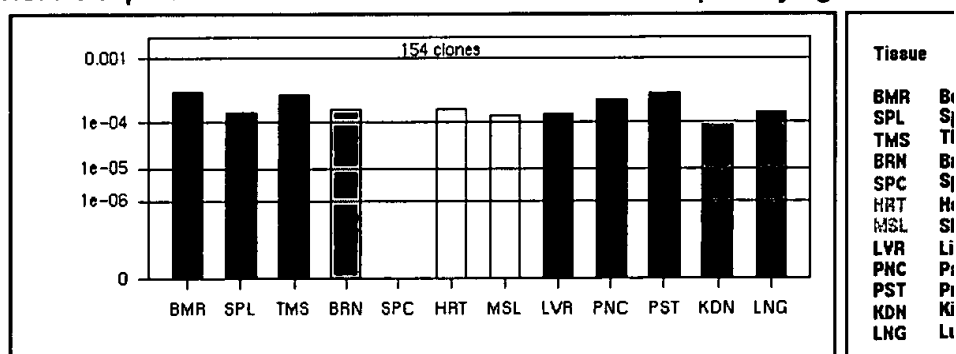
DOTS assembly:

[DT.87008863](#) [DT.91778195](#) [DT.95343265](#) [DT.97868449](#) [DT.95296185](#) [DT.95295959](#) [DT.97868444](#) [DT.40126798](#) [DT.91778226](#) [DT.95378439](#) [DT.95285344](#) [DT.95295962](#) [DT.95296183](#) [DT.97864054](#) [DT.40115805](#)Unigene Cluster for HSPA5: (Build 155 Homo sapiens; Sep 23 2002)
heat shock 70kDa protein 5 (glucose-regulated protein, 78kDa)
[Hs.75410](#) [\[show with all ESTs\]](#)Unigene Representative Sequence: [NM_005347](#)**Sequences**(GenBank/EMBL/DDBJ
Accessions According to
[Unigene](#) or [GenBank](#), RefSeq
According to [LocusLink](#),
Assembly According to [MIPS](#)
and/or [DOTS](#))

HSPA5 expression in normal human tissues based on proprietary W.I.S DNA

Expression in Human Tissues
(According to proprietary W.I.S
DNA array results (GeneNOTE),
[UniGene](#) and/or [SOURCE](#))

HSPA5 expression in normal human tissues based on quantifying ESTs for

SOURCE GeneReport for Unigene cluster [Hs.75410](#)**Similar Genes in Other
Organisms**(According to MGD Oct 18 2002
Stony Brook
[C.elegans-H.sapiens Alignment](#)
[Database](#) and/or [euGenes](#))**Homologues:**

	gene	locus	description
mouse (MGD)	Hspa5	2 (22.50 cM)	heat shock 70kD protein 5 (glucose-regulated protein, 78kD)
C. elegans (Stony Brook)	F43E2.8	--	description: Caenorhabditis elegans cosmids complete sequence

<div>SNPs/Variants</div> <div>(According to theNCBI SNP Database and to <u>SWISS-PROT</u>)</div>	Variants: <u>SWISS-PROT: GR78 HUMAN</u>					
	NCBI SNPs: 8 selected, not withdrawn, single nucleotide mutations are shown here					
	Genomic Data					
	SNP ID	Contig Accession	Position in Contig	Strand	5' Flanking Sequence*	3' Flanking :
	rs12009	NT_029366.6	1388056	-	AGGCCAAGCCCAATA	AGCCATTAA
	rs7922	NT_029366.6	1389486	-	CTGCTATAGCCTAAG	GGCTGTTT
	rs430397	NT_029366.6	1391872	-	CATCACAGTAACCAT	TCTTTTTT
	rs387491	NT_029366.6	1394201	+	CAGTCCAGCCACAGG	CGTAGCAC
	rs424676	NT_029366.6	1394200	+	GCAGTCCAGCCACAG	CCGTAGCA
	rs8759	NT_029366.6	1389404	-	GCCATCTTAAAAAGC	GGTAAAAA
rs589306	NT_029366.6	1392756	-	tttttttttttt	aatttcag	
rs391957	NT_029366.6	1394777	+	GGATCTGAAACTTTT	CTTCTCTA	
* Lower case letters indicate repetitive or low-complexity sequence						
All NCBI SNPs in <u>HSPA5</u>						
<div>Disorders & Mutations</div> <div>(in which this Gene is Involved, According to OMIM, <u>SWISS-PROT</u>, <u>Genatlas</u>, <u>GeneClinics</u>, <u>HGMD</u>, <u>BCGD</u>, and/or <u>TGDB</u>.)</div>	--					
<div>Medical News</div> <div>(Possibly Related Articles in <u>Doctor's Guide</u>)</div>	--					
<div>Research Articles</div> <div>(in <u>PubMed</u>)</div>	<div><div><div>Search PubMed for HSPA5</div></div><div>to find abstracts of research articles</div></div>					
<div>HSPA5 in Other Genome Wide Resources:</div> <div>(According to <u>GDB</u>, <u>LocusLink</u>, <u>euGenes</u>, <u>Ensembl</u> and/or <u>GeneLynx</u>)</div>	<div><div><div><u>GDB: 127962</u></div><div><u>LocusLink: 3309</u></div><div><u>euGenes: HUgn3309</u></div><div><u>Ensembl: ENSG</u></div></div></div>					
<div>HSPA5 in General Databases, Limited Scope</div> <div>(According to <u>HUGE</u>)</div>	--					
<div>HSPA5 in Specialized Databases</div> <div>(According to <u>ATLAS</u>, <u>GENATLAS</u>, <u>HORDE</u>, <u>IMGT</u>, <u>MTDB</u>, <u>LEIDEN</u> and/or <u>SWISS-PROT</u>)</div>	<div><div><div><i>name</i></div><div>Genatlas biochemistry entry for HSPA5: glucose regulated protein (78kDa),HSP of PPP1CC2</div></div></div>					
<div>Services</div> <div>(According to <u>RZPD</u>)</div>	<div><div><div><u>Search RZPD for clones of HSPA5</u></div><div>Clone collection at the German Human Gen</div></div></div>					

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Developed at the [Crown Human Genome Center & Weizmann Institute of Science](#)

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NiceProt View of SWISS-PROT: P11021

General information about the entry

Entry name	GR78_HUMAN
Primary accession number	P11021
Secondary accession number	Q9NPF1
Entered in SWISS-PROT in	Release 11, July 1989
Sequence was last modified in	Release 40, October 2001
Annotations were last modified in	Release 41, June 2002

Name and origin of the protein

Protein name	78 kDa glucose-regulated protein [Precursor]
Synonyms	GRP 78 Immunoglobulin heavy chain binding protein BIP Endoplasmic reticulum lumenal Ca²⁺ binding protein grp78
Gene name	HSPA5 or GRP78
From	Homo sapiens (Human) [TaxID: 9606]
Taxonomy	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

References

[1] SEQUENCE FROM NUCLEIC ACID.

MEDLINE=88283347; PubMed=2840249;

Ting J., Lee A.S.;

"Human gene encoding the 78,000-dalton glucose-regulated protein and its pseudogene: structure, conservation, and regulation.";

DNA 7:275-286(1988).

[2] SEQUENCE FROM NUCLEIC ACID.

TISSUE=Cervical carcinoma;

Chao C.C.K.;

Submitted (DEC-1995) to the EMBL/GenBank/DDBJ databases.

[3] SEQUENCE FROM NUCLEIC ACID.

TISSUE=Fibroblast;

Hansen J.J., Nielsen M.N., Jorgensen M.M., Gregersen N., Bolund L.;

"Grp78 is involved in the quality control of the LDL-receptor.";

Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.

[4] SEQUENCE FROM NUCLEIC ACID.

Bermudez-Fajardo A., Llewellyn D.H., Campbell A.K., Errington R.R.;

"Sequence differences between human grp78/BiP isolated from HeLa cells and previously reported human sequences.";

Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.

[5] SEQUENCE OF 1-25 FROM NUCLEIC ACID.

MEDLINE=93126087; PubMed=1480470;

Chao C.C.K., Lin-Chao S.;

"A direct-repeat sequence of the human BiP gene is required for A23187-mediated inducibility and an inducible nuclear factor binding.";

Nucleic Acids Res. 20:6481-6485(1992).

[6] SEQUENCE OF 22-38.

TISSUE=Breast carcinoma;

MEDLINE=97295304; PubMed=9150946;

Rasmussen R.K., Ji H., Eddes J.S., Moritz R.L., Reid G.E., Simpson R.J., Dorow D.S.;

"Two-dimensional electrophoretic analysis of human breast carcinoma proteins: mapping of proteins that bind to the SH3 domain of mixed lineage kinase MLK2.";

Electrophoresis 18:588-598(1997).

[7] SEQUENCE OF 19-40.

TISSUE=Colon carcinoma;

MEDLINE=97295306; PubMed=9150948;

Ji H., Reid G.E., Moritz R.L., Eddes J.S., Burgess A.W., Simpson R.J.;

"A two-dimensional gel database of human colon carcinoma proteins.";

Electrophoresis 18:605-613(1997).

Comments

- **FUNCTION:** PROBABLY PLAYS A ROLE IN FACILITATING THE ASSEMBLY OF MULTIMERIC PROTEIN COMPLEXES INSIDE THE ER.
- **SUBCELLULAR LOCATION:** Endoplasmic reticulum lumen.
- **SIMILARITY:** BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.

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Cross-references

EMBL	M19645; AAA52614.1; -. X87949; CAA61201.1; -. AJ271729; CAB71335.1; -. AF216292; AAF42836.1; -. X59969; CAA42595.1; -.
PIR	A29821; A29821.
HSSP	P19120; 3HSC.
SWISS-2DPAGE	P11021; HUMAN.
PMMA-2DPAGE	P11021; -.
PHCI-2DPAGE	P11021; -.
Siena-2DPAGE	P11021; -.
Genew	HGNC:5238; HSPA5.
MIM	138120 .
GeneCards	HSPA5.
GeneLynx	HSPA5; Homo sapiens.
InterPro	IPR000886; ER_target. IPR001023; Hsp70.
Pfam	PF00012; HSP70; 1.
PRINTS	PR00301; HEATSHOCK70.
ProDom	PD000089; Hsp70; 1. [Domain structure / List of seq. sharing at least 1 domain].
PROSITE	PS00014; ER_TARGET; 1. PS00297; HSP70_1; 1. PS00329; HSP70_2; 1. PS01036; HSP70_3; 1.
Implicit links to	SOURCE; Ensembl; BLOCKS; ProtoNet; ProtoMap; PRESAGE; DIP; ModBase.

Keywords

ATP-binding; Endoplasmic reticulum; Signal.

Features

Key	From	To	Length	Description
SIGNAL	1	18	18	
CHAIN	19	654	636	78 KDA GLUCOSE-REGULATED PROTEIN.
SITE	651	654	4	PREVENT SECRETION FROM ER.
CONFLICT	297	297		MISSING (IN REF. 1 AND 2).
CONFLICT	418	418		D -> H (IN REF. 1 AND 2).
CONFLICT	439	439		R -> S (IN REF. 1 AND 2).
CONFLICT	447	447		K -> N (IN REF. 1 AND 2).

Sequence information

Length: **654 AA** [This is the length of the unprocessed precursor]

Molecular weight: **72333 Da** [This is the MW of the unprocessed precursor]

CRC64: **59B7D8D85BC32A00** [This is a checksum on the sequence]

10	20	30	40	50	60
MKLSLVAAML	LLLSAARAE	EDKKEDVGT	VGIDLGTTYS	CVGVFKNGRV	EIIANDQGNR
70	80	90	100	110	120
ITPSYVAFTP	EGERLIGDAA	KNQLTSNPEN	TVFDAKRLIG	RTWNDPSVQQ	DIKFLPFKVV
130	140	150	160	170	180
EKKTKPYIQV	DIGGGQTKTF	APEEISAMVL	TKMKETAEAY	LGKKVTHAVV	TVPAYFNDAQ
190	200	210	220	230	240
RQATKDAGTI	AGLNMRIIN	EPTAAAIAYG	LDKREGEKNI	LVFDLGGGTF	DVSLLTIDNG
250	260	270	280	290	300
VFEVVATNGD	THLGGEDFDQ	RVMEHFILY	KKKTGKDVRK	DNRAVQKLRR	EVEKAKRALS
310	320	330	340	350	360
SQHQAIEIE	SFYEGEDFSE	TLTRAKFEEL	NMDLFRSTMK	PVQKVLESD	LKKSDDIDEIV
370	380	390	400	410	420
LVGGSTRIPK	IQQLVKEFFN	GKEPSRGINP	DEAVAYGAAV	QAGVLSGDQD	TGDLVLLDVC
430	440	450	460	470	480
PLTLGIETVG	GVMTKLIPRN	TVVPTKKSQI	FSTASDNQPT	VTIKVYEGER	PLTKDNHLLG
490	500	510	520	530	540
TFDLTGIPPA	PRGVPQIEVT	FEIDVNGILR	VTAEDKGTGN	KNKITITNDQ	NRLTPEEIER
550	560	570	580	590	600
MVNDAEKFAE	EDKKLKERID	TRNELESYAY	SLKNQIGDKE	KLGGKLSSSD	KETMEKAVEE
610	620	630	640	650	
KIEWLESHQD	ADIEDFKAKK	KELEEIVQPI	ISKLYGSAGP	PPTGEEDTAE	KDEL